

0425

#4



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/047,412A

DATE: 04/26/2002
TIME: 11:45:53

Input Set : A:\30780DIV1 revised sequence listing v2.txt
Output Set: N:\CRF3\04262002\J047412A.raw

3 <110> APPLICANT: Levin, Joshua Z.
4 Budziszewski, Gregory J.
5 Potter, Sharon L.
6 Wegrich, Lynette M.
8 <120> TITLE OF INVENTION: Herbicide Target Genes and Methods
10 <130> FILE REFERENCE: PB/5-30780DIV
12 <140> CURRENT APPLICATION NUMBER: 10/047,412A
C--> 13 <141> CURRENT FILING DATE: 2002-04-11
15 <160> NUMBER OF SEQ ID NOS: 29
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1119
21 <212> TYPE: DNA
22 <213> ORGANISM: Arabidopsis thaliana
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1119)
28 <400> SEQUENCE: 1

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31	1 5 10 15	
33	aag aag aag att aaa gat gtt gtt ctt aag gct gag atg ttt gca ccg	96
34	Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe Ala Pro	
35	20 25 30	
37	gat gct ctt gag ctt gaa gaa gag cag tgg ata aag caa gaa gaa aca	144
38	Asp Ala Leu Glu Leu Glu Glu Gln Trp Ile Lys Gln Glu Glu Thr	
39	35 40 45	
41	atg cgt tac ttt gat tta tgg gat gat ccc gct aaa tct gat gag att	192
42	Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp Glu Ile	
43	50 55 60	
45	ctt ctc aaa tta gct gat cga gct aaa gca gtc gat tcc ctc aaa gac	240
46	Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu Lys Asp	
47	65 70 75 80	
49	ctc aaa tac aag gct gaa gaa gct aag ctg atc ata caa ttg ggt gag	288
50	Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu Gly Glu	
51	85 90 95	
53	atg gat gct ata gat tac agt ctc ttt gag caa gcc tat gat tca tca	336
54	Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp Ser Ser	
55	100 105 110	
57	ctc gat gta agt aga tcg ttg cat cac tat gag atg tct aag ctt ctt	384
58	Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys Leu Leu	
59	115 120 125	
61	agg gat caa tat gac gct gaa ggc gct tgt atg att atc aaa tct gga	432

Input Set : A:\30780DIV1 revised sequence listing v2.txt
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62 Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys Ser Gly
63 130 135 140 480
65 tct cca ggc gca aaa tct cag ata tgg aca gag caa gtt gta agt atg
66 Ser Pro Gly Ala Lys Ser Gln Ile Trp Thr Glu Gln Val Val Ser Met
67 145 150 155 160 528
69 tat atc aaa tgg gca gaa agg cta ggc caa aac gcg cgg gtg gct gag
70 Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn Ala Arg Val Ala Glu
71 165 170 175 576
73 aaa tgt agt tta ttg agt aat aaa agt ggc gta agt tca gcc acg ata
74 Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val Ser Ser Ala Thr Ile
75 180 185 190 624
77 gag ttt gaa ttc gag ttt gct tat ggt tat ctc tta ggt gag cga ggt
78 Glu Phe Glu Phe Ala Tyr Gly Tyr Leu Leu Gly Glu Arg Gly 624
79 195 200 205 672
81 gtg cac cgc ctt atc ata agt tcc act tct aat gag gaa tgt tca gcg
82 Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn Glu Glu Cys Ser Ala
83 210 215 220 720
85 act gtt gat atc ata cca cta ttc ttg aga gca tct cct gat ttt gaa
86 Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala Ser Pro Asp Phe Glu
87 225 230 235 240 768
89 gta aag gaa ggt gat ttg att gta tcg tat cct gca aaa gag gat cac
90 Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro Ala Lys Glu Asp His
91 245 250 255 816
93 aaa ata gct gag aat atg gtt tgt atc cac cat att ccg agt gga gta
94 Lys Ile Ala Glu Asn Met Val Cys Ile His His Ile Pro Ser Gly Val
95 260 265 270 864
97 aca cta caa tct tca gga gaa aga aac cgg ttt gca aac agg atc aaa
98 Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe Ala Asn Arg Ile Lys
99 275 280 285 912
101 gct cta aac cgg ttg aag gcg aag cta ctt gtg ata gca aaa gag caa
102 Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val Ile Ala Lys Glu Gln
103 290 295 300 960
105 aag gtt tcg gat gta aat aaa atc gac agc aag aac att ttg gaa ccg
106 Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys Asn Ile Leu Glu Pro
107 305 310 315 320 1008
109 cgg gaa gaa acc agg agt tat gtc tct aag ggt cac aag atg gtg gtt
110 Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly His Lys Met Val Val
111 325 330 335 1056
113 gat aga aaa acc ggt tta gag att ctg gac ctg aaa tcg gtc ttg gat
114 Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu Lys Ser Val Leu Asp
115 340 345 350 1104
117 gga aac att gga cca ctc ctt gga gct cat att agc atg aga aga tca
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119 355 360 365 1119
121 att gat gcg att tag
122 Ile Asp Ala Ile
123 370
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 372

Input Set : A:\30780DIV1 revised sequence listing v2.txt
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128 <212> TYPE: PRT
129 <213> ORGANISM: Arabidopsis thaliana
131 <400> SEQUENCE: 2
132 Met Asp Asp Met Asp Thr Val Tyr Lys Gln Leu Gly Leu Phe Ser Leu
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134 Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe Ala Pro
135 20 25 30
136 Asp Ala Leu Glu Leu Glu Glu Gln Trp Ile Lys Gln Glu Glu Thr
137 35 40 45
138 Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp Glu Ile
139 50 55 60
140 Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu Lys Asp
141 65 70 75 80
142 Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu Gly Glu
143 85 90 95
144 Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp Ser Ser
145 100 105 110
146 Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys Leu Leu
147 115 120 125
148 Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys Ser Gly
149 130 135 140
150 Ser Pro Gly Ala Lys Ser Gln Ile Trp Thr Glu Gln Val Val Ser Met
151 145 150 155 160
152 Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn Ala Arg Val Ala Glu
153 165 170 175
154 Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val Ser Ser Ala Thr Ile
155 180 185 190
156 Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu Leu Gly Glu Arg Gly
157 195 200 205
158 Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn Glu Glu Cys Ser Ala
159 210 215 220
160 Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala Ser Pro Asp Phe Glu
161 225 230 235 240
162 Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro Ala Lys Glu Asp His
163 245 250 255
164 Lys Ile Ala Glu Asn Met Val Cys Ile His His Ile Pro Ser Gly Val
165 260 265 270
166 Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe Ala Asn Arg Ile Lys
167 275 280 285
168 Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val Ile Ala Lys Glu Gln
169 290 295 300
170 Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys Asn Ile Leu Glu Pro
171 305 310 315 320
172 Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly His Lys Met Val Val
173 325 330 335
174 Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu Lys Ser Val Leu Asp
175 340 345 350
176 Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile Ser Met Arg Arg Ser
177 355 360 365

Input Set : A:\30780DIV1 revised sequence listing v2.txt
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178 Ile Asp Ala Ile
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183 <210> SEQ ID NO: 3
184 <211> LENGTH: 1458
185 <212> TYPE: DNA
186 <213> ORGANISM: Arabidopsis thaliana
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (1)..(1458)
192 <400> SEQUENCE: 3
193 atg gca act ctt gaa gat tct ttc ctt gct gat ttg gac gag tta tct 48
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195 1 5 10 15
197 gac aat gaa gca gaa ttg gac gag aat gat ggt gat gtt gga aag gaa 96
198 Asp Asn Glu Ala Glu Leu Asp Glu Asn Asp Gly Asp Val Gly Lys Glu
199 20 25 30
201 gaa gaa gat gtt gat atg gat atg gct gat tta gag aca ctt aac tat 144
202 Glu Glu Asp Val Asp Met Asp Met Ala Asp Leu Glu Thr Leu Asn Tyr
203 35 40 45
205 gat gat ctc gat aat gtt tct aag ctg cag aag agt cag aga tat gct 192
206 Asp Asp Leu Asp Asn Val Ser Lys Leu Gln Lys Ser Gln Arg Tyr Ala
207 50 55 60
209 gat att atg cat aaa gta gag gag gct ctt ggg aaa gat tct gat gga 240
210 Asp Ile Met His Lys Val Glu Glu Ala Leu Gly Lys Asp Ser Asp Gly
211 65 70 75 80
213 gct gag aaa gga act gtc ttg gaa gat gat cct gag tat aag ctt att 288
214 Ala Glu Lys Gly Thr Val Leu Glu Asp Asp Pro Glu Tyr Lys Leu Ile
215 85 90 95
217 gtg gat tgt aat cag ctt tcg gtc gat att gag aat gaa atc gtt att 336
218 Val Asp Cys Asn Gln Leu Ser Val Asp Ile Glu Asn Glu Ile Val Ile
219 100 105 110
221 gtc cac aac ttt atc aaa gac aag tac aag ctt aag ttt caa gag ctt 384
222 Val His Asn Phe Ile Lys Asp Lys Tyr Lys Leu Lys Phe Gln Glu Leu
223 115 120 125
225 gag tcg ttg gtt cat cac cct att gac tat gca tgt gtt gtg aag aag 432
226 Glu Ser Leu Val His His Pro Ile Asp Tyr Ala Cys Val Val Lys Lys
227 130 135 140
229 att ggg aat gag acg gat ttg gct ctt gtt gat ctc gct gac ctt ctt 480
230 Ile Gly Asn Glu Thr Asp Leu Ala Leu Val Asp Leu Ala Asp Leu Leu
231 145 150 155 160
233 cct tca gct att atc atg gtt tca gtt act gct tta act acg aaa 528
234 Pro Ser Ala Ile Ile Met Val Val Ser Val Thr Ala Leu Thr Thr Lys
235 165 170 175
237 ggg agt gca ctg cca gag gat gtt ttg caa aag gtg tta gag gct tgt 576
238 Gly Ser Ala Leu Pro Glu Asp Val Leu Gln Lys Val Leu Glu Ala Cys
239 180 185 190
241 gat cgg gct tta gat ctt gat tcc gca agg aag aag gtc ctt gag ttt 624
242 Asp Arg Ala Leu Asp Leu Asp Ser Ala Arg Lys Lys Val Leu Glu Phe
243 195 200 205

Input Set : A:\30780DIV1 revised sequence listing v2.txt
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245 gtt gaa agt aag atg gga tct att gca cct aat ctt tct gct att gtt	672
246 Val Glu Ser Lys Met Gly Ser Ile Ala Pro Asn Leu Ser Ala Ile Val	
247 210 215 220	
249 ggg agt gct gtt gca gcc aaa ctc atg ggg act gct gga ggt ttg tca	720
250 Gly Ser Ala Val Ala Ala Lys Leu Met Gly Thr Ala Gly Gly Leu Ser	
251 225 230 235 240	
253 gca ctt gct aaa atg cct gcg tgt aat gtt caa gtt ctt ggc cac aag	768
254 Ala Leu Ala Lys Met Pro Ala Cys Asn Val Gln Val Leu Gly His Lys	
255 245 250 255	
257 agg aag aac ctt gct ggg ttt tct tct gca acg tct cag tcc cgt gtg	816
258 Arg Lys Asn Leu Ala Gly Phe Ser Ser Ala Thr Ser Gln Ser Arg Val	
259 260 265 270	
261 ggt tat ctg gag cag aca gag att tac caa agc acg cct cct gga ctt	864
262 Gly Tyr Leu Glu Gln Thr Glu Ile Tyr Gln Ser Thr Pro Pro Gly Leu	
263 275 280 285	
265 cag gct cgc gct ggc agg ctc gtg gct gca aaa tca act ttg gca gca	912
266 Gln Ala Arg Ala Gly Arg Leu Val Ala Ala Lys Ser Thr Leu Ala Ala	
267 290 295 300	
269 aga gtt gat gct act aga ggg gat ccg tta ggg ata agt gga aaa gct	960
270 Arg Val Asp Ala Thr Arg Gly Asp Pro Leu Gly Ile Ser Gly Lys Ala	
271 305 310 315 320	
273 ttc agg gag gag atc cgt aag aag att gag aaa tgg caa gaa cct cct	1008
274 Phe Arg Glu Glu Ile Arg Lys Ile Glu Lys Trp Gln Glu Pro Pro	
275 325 330 335	
277 cct gca aga cag cct aag cca ctt cct gtt cct gat tct gaa ccg aag	1056
278 Pro Ala Arg Gln Pro Lys Pro Leu Pro Val Pro Asp Ser Glu Pro Lys	
279 340 345 350	
281 aaa aga agg ggt ggt cgc cgt cta aga aaa atg aaa gaa agg tat caa	1104
282 Lys Arg Arg Gly Gly Arg Arg Leu Arg Lys Met Lys Glu Arg Tyr Gln	
283 355 360 365	
285 gta aca gat atg agg aag ctg gcc aac aga atg gcg ttt ggt aca cct	1152
286 Val Thr Asp Met Arg Lys Leu Ala Asn Arg Met Ala Phe Gly Thr Pro	
287 370 375 380	
289 gaa gag agc tcc ctc ggt gat gga cta gga gaa ggt tat gga atg ctt	1200
290 Glu Glu Ser Ser Leu Gly Asp Gly Leu Gly Glu Gly Tyr Gly Met Leu	
291 385 390 395 400	
293 ggc cag gca gga agc aac agg ctg cga gta tcc agt gtt ccg agc aag	1248
294 Gly Gln Ala Gly Ser Asn Arg Leu Arg Val Ser Ser Val Pro Ser Lys	
295 405 410 415	
297 ctt aag att aat gct aag gtc gcc aaa aag ctt aaa gaa agg cag tat	1296
298 Leu Lys Ile Asn Ala Lys Val Ala Lys Lys Leu Lys Glu Arg Gln Tyr	
299 420 425 430	
301 gcg ggt ggt gcg act acc tct ggt ttg aca tcg agc ctg gct ttc act	1344
302 Ala Gly Gly Ala Thr Thr Ser Gly Leu Thr Ser Ser Leu Ala Phe Thr	
303 435 440 445	
305 cct gtg cag gga ata gag ttg tgc aat cct cag cag gct tta gga tta	1392
306 Pro Val Gln Gly Ile Glu Leu Cys Asn Pro Gln Gln Ala Leu Gly Leu	
307 450 455 460	
309 gga agt ggg act caa agc act tac ttc tca gag tca gga acc ttc tcg	1440

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/047,412A

DATE: 04/26/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 19

Seq#:29; Xaa Pos. 39,155,162,187,465